

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/537, 746 A.
Source: PLT
Date Processed by STIC: 02/02/2006

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PCT

RAW SEQUENCE LISTING

DATE: 02/02/2006

PATENT APPLICATION: US/10/537,746A

TIME: 11:45:52

Input Set : A:\Sequence.ST25.txt

Output Set: N:\CRF4\02022006\J537746A.raw

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3 <110> APPLICANT: De Maria, Leonardo
4     Svendsen, Allan
5     Borchert, Torben Vedel
6     Christensen, Lars Lehmann Hylling
7     Larsen, Sine
8     Ryttergaard, Carsten
10 <120> TITLE OF INVENTION: Galactanase Variants
12 <130> FILE REFERENCE: 10319.204-US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/537,746A
C--> 14 <141> CURRENT FILING DATE: 2005-06-06
14 <160> NUMBER OF SEQ ID NOS: 9
16 <170> SOFTWARE: PatentIn version 3.3
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 332
20 <212> TYPE: PRT
21 <213> ORGANISM: Myceliophthora thermophila
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25 <221> NAME/KEY: mat_peptide
26 <222> LOCATION: (1)..()
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35          20          25          30
38 Glu Asn Ile Leu Ala Ala Asn Gly Val Asn Thr Val Arg Gln Arg Val
39          35          40          45
42 Trp Val Asn Pro Ala Asp Gly Asn Tyr Asn Leu Asp Tyr Asn Ile Ala
43          50          55          60
46 Ile Ala Lys Arg Ala Lys Ala Ala Gly Leu Gly Val Tyr Ile Asp Phe
47 65          70          75          80
50 His Tyr Ser Asp Thr Trp Ala Asp Pro Ala His Gln Thr Met Pro Ala
51          85          90          95
54 Gly Trp Pro Ser Asp Ile Asp Asn Leu Ser Trp Lys Leu Tyr Asn Tyr
55          100         105         110
58 Thr Leu Asp Ala Ala Asn Lys Leu Gln Asn Ala Gly Ile Gln Pro Thr
59          115         120         125
62 Ile Val Ser Ile Gly Asn Glu Ile Arg Ala Gly Leu Leu Trp Pro Thr
63          130         135         140
66 Gly Arg Thr Glu Asn Trp Ala Asn Ile Ala Arg Leu Leu His Ser Ala
67 145         150         155         160
70 Ala Trp Gly Ile Lys Asp Ser Ser Leu Ser Pro Lys Pro Lys Ile Met
71          165         170         175
74 Ile His Leu Asp Asn Gly Trp Asp Trp Gly Thr Gln Asn Trp Trp Tyr

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75          180          185          190
78 Thr Asn Val Leu Lys Gln Gly Thr Leu Glu Leu Ser Asp Phe Asp Met
79          195          200          205
82 Met Gly Val Ser Phe Tyr Pro Phe Tyr Ser Ser Ser Ala Thr Leu Ser
83          210          215          220
86 Ala Leu Lys Ser Ser Leu Asp Asn Met Ala Lys Thr Trp Asn Lys Glu
87 225          230          235          240
90 Ile Ala Val Val Glu Thr Asn Trp Pro Ile Ser Cys Pro Asn Pro Arg
91          245          250          255
94 Tyr Ser Phe Pro Ser Asp Val Lys Asn Ile Pro Phe Ser Pro Glu Gly
95          260          265          270
98 Gln Thr Thr Phe Ile Thr Asn Val Ala Asn Ile Val Ser Ser Val Ser
99          275          280          285
102 Arg Gly Val Gly Leu Phe Tyr Trp Glu Pro Ala Trp Ile His Asn Ala
103          290          295          300
106 Asn Leu Gly Ser Ser Cys Ala Asp Asn Thr Met Phe Ser Gln Ser Gly
107 305          310          315          320
110 Gln Ala Leu Ser Ser Leu Ser Val Phe Gln Arg Ile
111          325          330
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117 <213> ORGANISM: Humicola insolens
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122 <222> LOCATION: (1)..()
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134 Glu Tyr Ile Leu Ala Glu Asn Gly Val Asn Met Val Arg Gln Arg Val
135          35          40          45
138 Trp Val Asn Pro Trp Asp Gly Asn Tyr Asn Leu Asp Tyr Asn Ile Gln
139          50          55          60
142 Leu Ala Arg Arg Ala Lys Ala Ala Gly Leu Gly Leu Tyr Ile Asn Phe
143 65          70          75          80
146 His Tyr Ser Asp Thr Trp Ala Asp Pro Ala His Gln Thr Thr Pro Ala
147          85          90          95
150 Gly Trp Pro Ser Asp Ile Asn Asn Leu Ala Trp Lys Leu Tyr Asn Tyr
151          100          105          110
154 Thr Leu Asp Ser Met Asn Arg Phe Ala Asp Ala Gly Ile Gln Val Asp
155          115          120          125
158 Ile Val Ser Ile Gly Asn Glu Ile Thr Gln Gly Leu Leu Trp Pro Leu
159          130          135          140
162 Gly Lys Thr Asn Asn Trp Tyr Asn Ile Ala Arg Leu Leu His Ser Ala
163 145          150          155          160
166 Ala Trp Gly Val Lys Asp Ser Arg Leu Asn Pro Lys Pro Lys Ile Met
167          165          170          175

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170 Val His Leu Asp Asn Gly Trp Asn Trp Asp Thr Gln Asn Trp Trp Tyr
171      180      185      190
174 Thr Asn Val Leu Ser Gln Gly Pro Phe Glu Met Ser Asp Phe Asp Met
175      195      200      205
178 Met Gly Val Ser Phe Tyr Pro Phe Tyr Ser Ala Ser Ala Thr Leu Asp
179      210      215      220
182 Ser Leu Arg Arg Ser Leu Asn Asn Met Val Ser Arg Trp Gly Lys Glu
183 225      230      235      240
186 Val Ala Val Val Glu Thr Asn Trp Pro Thr Ser Cys Pro Tyr Pro Arg
187      245      250      255
190 Tyr Gln Phe Pro Ala Asp Val Arg Asn Val Pro Phe Ser Ala Ala Gly
191      260      265      270
194 Gln Thr Gln Tyr Ile Gln Ser Val Ala Asn Val Val Ser Ser Val Ser
195      275      280      285
198 Lys Gly Val Gly Leu Phe Tyr Trp Glu Pro Ala Trp Ile His Asn Ala
199      290      295      300
202 Asn Leu Gly Ser Ser Cys Ala Asp Asn Thr Met Phe Thr Pro Ser Gly
203 305      310      315      320
206 Gln Ala Leu Ser Ser Leu Ser Val Phe His Arg Ile
207      325      330
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211 <211> LENGTH: 334
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213 <213> ORGANISM: Aspergillus aculeatus
216 <220> FEATURE:
217 <221> NAME/KEY: mat_peptide
218 <222> LOCATION: (1)..()
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226 Asp Glu Gly Tyr Ser Tyr Lys Asn Leu Asn Gly Gln Thr Gln Ala Leu
227      20      25      30
230 Glu Thr Ile Leu Ala Asp Ala Gly Ile Asn Ser Ile Arg Gln Arg Val
231      35      40      45
234 Trp Val Asn Pro Ser Asp Gly Ser Tyr Asp Leu Asp Tyr Asn Leu Glu
235      50      55      60
238 Leu Ala Lys Arg Val Lys Ala Ala Gly Met Ser Leu Tyr Leu Asp Leu
239 65      70      75      80
242 His Leu Ser Asp Thr Trp Ala Asp Pro Ser Asp Gln Thr Thr Pro Ser
243      85      90      95
246 Gly Trp Ser Thr Thr Asp Leu Gly Thr Leu Lys Trp Gln Leu Tyr Asn
247      100      105      110
250 Tyr Thr Leu Glu Val Cys Asn Thr Phe Ala Glu Asn Asp Ile Asp Ile
251      115      120      125
254 Glu Ile Ile Ser Ile Gly Asn Glu Ile Arg Ala Gly Leu Leu Trp Pro
255      130      135      140
258 Leu Gly Glu Thr Ser Ser Tyr Ser Asn Ile Gly Ala Leu Leu His Ser
259 145      150      155      160
262 Gly Ala Trp Gly Val Lys Asp Ser Asn Leu Ala Thr Thr Pro Lys Ile

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263          165          170          175
266 Met Ile His Leu Asp Asp Gly Trp Ser Trp Asp Gln Gln Asn Tyr Phe
267          180          185          190
270 Tyr Glu Thr Val Leu Ala Thr Gly Glu Leu Leu Ser Thr Asp Phe Asp
271          195          200          205
274 Tyr Phe Gly Val Ser Tyr Tyr Pro Phe Tyr Ser Ala Ser Ala Thr Leu
275          210          215          220
278 Ala Ser Leu Lys Thr Ser Leu Ala Asn Leu Gln Ser Thr Tyr Asp Lys
279 225          230          235          240
282 Pro Val Val Val Val Glu Thr Asn Trp Pro Val Ser Cys Pro Asn Pro
283          245          250          255
286 Ala Tyr Ala Phe Pro Ser Asp Leu Ser Ser Ile Pro Phe Ser Val Ala
287          260          265          270
290 Gly Gln Gln Glu Phe Leu Glu Lys Leu Ala Ala Val Val Glu Ala Thr
291          275          280          285
294 Thr Asp Gly Leu Gly Val Tyr Tyr Trp Glu Pro Ala Trp Ile Gly Asn
295          290          295          300
298 Ala Gly Leu Gly Ser Ser Cys Ala Asp Asn Leu Met Val Asp Tyr Thr
299 305          310          315          320
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303          325          330
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307 <211> LENGTH: 399
308 <212> TYPE: PRT
309 <213> ORGANISM: Bacillus licheniformis
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317 Val Ser Gly Leu Arg Lys Asp Phe Ile Lys Gly Val Asp Val Ser Ser
318          20          25          30
321 Ile Ile Ala Leu Glu Glu Ser Gly Val Ala Phe Tyr Asn Glu Ser Gly
322          35          40          45
325 Lys Lys Gln Asp Ile Phe Asn Thr Leu Lys Glu Ala Gly Val Asn Tyr
326          50          55          60
329 Val Arg Val Arg Ile Trp Asn Asp Pro Tyr Asp Ala Asn Gly Asn Gly
330 65          70          75          80
333 Tyr Gly Gly Gly Asn Asn Asp Leu Glu Lys Ala Ile Gln Ile Gly Lys
334          85          90          95
337 Arg Ala Asn Ala Asn Gly Met Lys Leu Leu Ala Asp Phe His Tyr Ser
338          100          105          110
341 Asp Phe Trp Ala Asp Pro Ala Lys Gln Lys Ala Pro Lys Ala Trp Ala
342          115          120          125
345 Asn Leu Asn Phe Glu Asp Lys Lys Thr Ala Leu Tyr Gln Tyr Thr Lys
346          130          135          140
349 Gln Ser Leu Lys Ala Met Lys Ala Ala Gly Ile Asp Ile Gly Met Val
350 145          150          155          160
353 Gln Val Gly Asn Glu Thr Asn Gly Gly Leu Ala Gly Glu Thr Asp Trp
354          165          170          175
357 Ala Lys Met Ser Gln Leu Phe Asn Ala Gly Ser Gln Ala Val Arg Glu

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358          180          185          190
361 Thr Asp Ser Asn Ile Leu Val Ala Leu His Phe Thr Asn Pro Glu Thr
362          195          200          205
365 Ser Gly Arg Tyr Ala Trp Ile Ala Glu Thr Leu His Arg His His Val
366          210          215          220
369 Asp Tyr Asp Val Phe Ala Ser Ser Tyr Tyr Pro Phe Trp His Gly Thr
370 225          230          235          240
373 Leu Lys Asn Leu Thr Ser Val Leu Thr Ser Val Ala Asp Thr Tyr Gly
374          245          250          255
377 Lys Lys Val Met Val Ala Glu Thr Ser Tyr Thr Tyr Thr Ala Glu Asp
378          260          265          270
381 Gly Asp Gly His Gly Asn Thr Ala Pro Lys Asn Gly Gln Thr Leu Asn
382          275          280          285
385 Asn Pro Val Thr Val Gln Gly Gln Ala Asn Ala Val Arg Asp Val Ile
386          290          295          300
389 Gln Ala Val Ser Asp Val Gly Glu Ala Gly Ile Gly Val Phe Tyr Trp
390 305          310          315          320
393 Glu Pro Ala Trp Ile Pro Val Gly Pro Ala His Arg Leu Glu Lys Asn
394          325          330          335
397 Lys Ala Leu Trp Glu Thr Tyr Gly Ser Gly Trp Ala Thr Ser Tyr Ala
398          340          345          350
401 Ala Glu Tyr Asp Pro Glu Asp Ala Gly Lys Trp Phe Gly Gly Ser Ala
402          355          360          365
405 Val Asp Asn Gln Ala Leu Phe Asp Phe Lys Gly Arg Pro Leu Pro Ser
406          370          375          380
409 Leu His Val Phe Gln Tyr Val Asp Thr Gly Thr Pro Phe Lys Asn
410 385          390          395

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413 <210> SEQ ID NO: 5
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415 <212> TYPE: DNA
416 <213> ORGANISM: Artificial Sequence
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419 <223> OTHER INFORMATION: Synthetic
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423 <221> NAME/KEY: misc_feature
424 <223> OTHER INFORMATION: Primer
426 <400> SEQUENCE: 5

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21

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433 <213> ORGANISM: Artificial Sequence
435 <220> FEATURE:
436 <223> OTHER INFORMATION: Synthetic
439 <220> FEATURE:
440 <221> NAME/KEY: misc_feature
441 <223> OTHER INFORMATION: Primer
443 <400> SEQUENCE: 6
444 gccgatcctt ctgatcagac catgcc

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26

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/537,746A

DATE: 02/02/2006

TIME: 11:45:53

Input Set : A:\Sequence.ST25.txt

Output Set: N:\CRF4\02022006\J537746A.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date